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Pyrimido[1,2-*a*]-purin-10(3*H*)-one, M₁G, is less prone to artifact than base oxidation

Yo-Chan Jeong, Jun Nakamura, Patricia B. Upton and James A. Swenberg*

Department of Environmental Sciences and Engineering, The University of North Carolina at Chapel Hill,
NC 27599-7431 USA

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ABSTRACT

Pyrimido[1,2-*a*]-purin-10(3*H*)-one (M₁G) is a secondary DNA damage product arising from primary reactive oxygen species (ROS) damage to membrane lipids or deoxyribose. The present study investigated conditions that might lead to artifactual formation or loss of M₁G during DNA isolation. The addition of antioxidants, DNA isolation at low temperature or non-phenol extraction methods had no statistically significant effect on the number of M₁G adducts measured in either control or positive control tissue samples. The number of M₁G adducts in nuclear DNA isolated from brain, liver, kidney, pancreas, lung and heart of control male rats were 0.8, 1.1, 1.1, 1.1, 1.8 and 4.2 M₁G/10⁸ nt, respectively. In rat liver tissue, the mitochondrial DNA contained a 2-fold greater number of M₁G adducts compared with nuclear DNA. Overall, the results from this study demonstrated that measuring M₁G is a reliable way to assess oxidative DNA damage because the number of M₁G adducts is significantly affected by the amount of ROS production, but not by DNA isolation procedures. In addition, this study confirmed that the background number of M₁G adducts reported in genomic DNA could have been overestimated by one to three orders of magnitude in previous reports.

INTRODUCTION

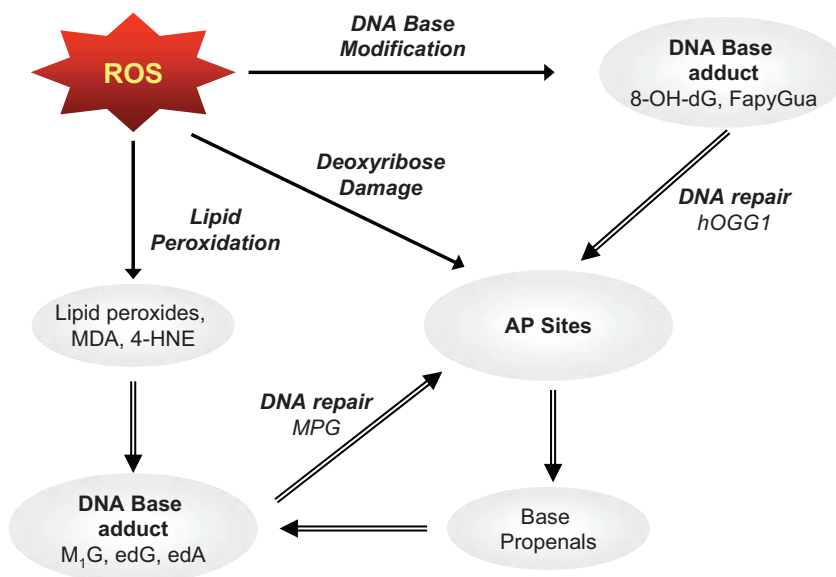
Reactive oxygen species (ROS), primarily superoxide anion radical (O₂⁻), are produced naturally from cellular sources such as mitochondria (1,2). In addition, humans, wildlife and laboratory animals are exposed daily to a complex mixture of chemicals, primarily via trace amounts present in food, drinking water or air, that can contribute to increased cellular ROS through a variety of mechanisms (3). Various oxidative DNA

lesions (Scheme 1) have been characterized and investigated for their role in the pathogenesis of adverse health effects and disease. One of the most studied biomarkers for oxidative DNA damage is 7,8-dihydro-8-OH-2'-deoxyguanosine (8-OH-dG). It is produced in relatively high amounts in cells and sensitive methods (i.e. LC-MS/MS) are available to measure it. However, the measurement of a single lesion such as 8-OH-dG as a biomarker might be misleading because it may not reflect the overall spectrum of DNA damage and its potential for mutations. In addition, the accumulation of oxidative DNA lesions could be affected by DNA repair, which is mediated by different pathways depending on the type of DNA lesion. Therefore, it is desirable to have multiple biomarkers to monitor oxidative DNA damage for investigating the role of ROS in the pathogenesis of diseases.

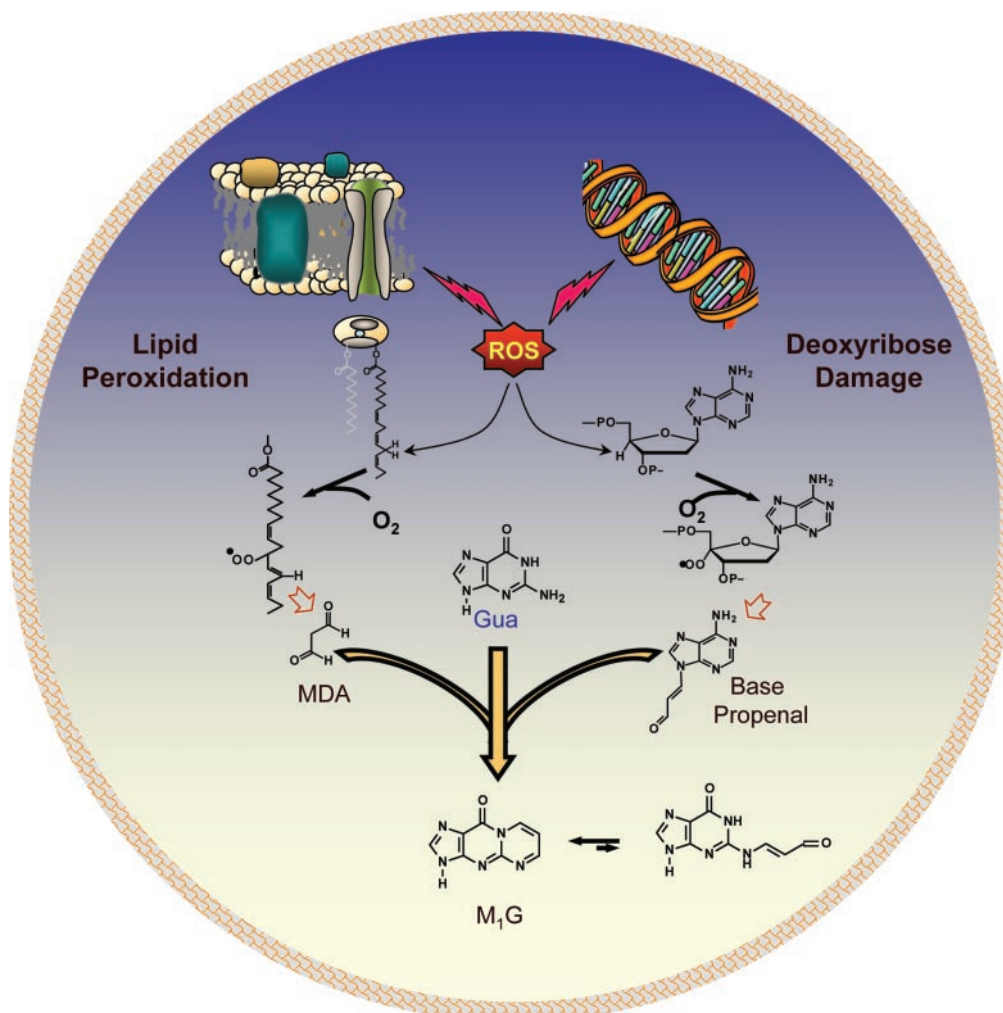
In addition to primary ROS lesions, a growing body of evidence supports that secondary DNA lesions produced from byproducts of primary DNA damage or lipid membrane oxidation play an important role in mutation (4,5) (Scheme 1). Pyrimido[1,2-*a*]-purin-10(3*H*)-one (M₁G) is one example of a secondary DNA lesion formed by primary ROS insults to lipid membranes or the DNA backbone (6–8) (Scheme 2). Malondialdehyde (MDA) from lipid peroxidation has been considered to be a key intermediate in M₁G formation (8). Dedon *et al.* (6) proposed an alternative pathway leading to M₁G formation via site-specific free radical attack on the DNA backbone.

Owing to its relatively high mutagenicity (9) and endogenous presence (10–14), considerable effort has been expended to establish a reliable method to measure M₁G adducts in genomic DNA. However, wide variation in the number of endogenous M₁G adducts has been reported for animal tissues. For example, different research groups (12,15–17) have reported between 4 and 300 M₁G/10⁷ nt from rat liver DNA. Such a wide variation in endogenous M₁G adducts poses great difficulty for using this biomarker in epidemiological studies. There is a critical need to establish normal and abnormal ranges of M₁G adducts as indicators of oxidative stress induced by diet, environmental or occupational exposures. A potential cause for such large discrepancies in the number

*To whom correspondence should be addressed. Tel: +1 919 966 6139; Fax: +1 919 966 6123; Email: james_swenberg@unc.edu
Correspondence may also be addressed to Yo-Chan Jeong. Tel: +1 919 966 6143; Fax: +1 919 966 6123; Email: yojeong@email.unc.edu



Scheme 1. Primary (\rightarrow) and secondary (\Rightarrow) DNA damage induced by ROS. FapyGua, 2,6-diamino-4-hydroxy-5-formamido-pyrimidine; hOGG1, 8-oxoguanine DNA glycosylase; 4-HNE, 4-hydroxy-2-nonenal; MPG, N-methylpurine-DNA-glycosylase; edG, ethenodeoxyguanosine; edA, 1,N⁶-ethenodeoxyadenosine.



Scheme 2. Formation of M₁G from ROS and equilibrium of M₁G.

of endogenous oxidative DNA lesions is artifacts that arise during DNA isolation and sample analysis. To investigate the role of M₁G in cancer development, our research group has established a novel analytical approach to measure M₁G using selective labeling with aldehyde reactive probe (18). This approach significantly reduced the artifacts during M₁G analysis by producing a stable conjugate, preventing artifactual formation or loss of adducts, enhancing sample enrichment, and finally measurement by LC-MS/MS. However, the production of artifacts during DNA isolation has not been investigated thoroughly for M₁G.

Years of research on primary oxidative DNA damage have shown that great care must be taken to avoid artifactual oxidative DNA damage during DNA isolation (19,20). Since M₁G is a product of ROS DNA damage, it is possible that artifactual formation of M₁G during DNA isolation could mask actual amounts of this lesion produced from either endogenous metabolism or chemical exposures. Furthermore, ring-opened M₁G, which is the dominant form in genomic DNA, is reactive toward amine compounds including Tris, a common buffering reagent used in DNA isolation (21,22). Conjugate formation between M₁G and amines could cause false negative results by decreasing the number of adducts recovered after DNA isolation. Therefore it is critical to establish a dependable DNA extraction protocol that minimizes errors in the measurement of M₁G. These considerations led us to investigating the influence on M₁G adduct quantification of artifacts during DNA isolation from tissue. In this study, artifactual formation of M₁G during DNA isolation was examined by comparing the following effects on the number of M₁G adducts: presence of added antioxidants; temperature during the work-up procedure; and different DNA isolation methods (Table 1). The loss of M₁G adducts during DNA isolation was tested by the addition of positive control DNA which had 25 times larger amounts of M₁G adducts than control calf thymus DNA. In addition, the quality of DNA was examined by monitoring DNA yield and the A₂₆₀/A₂₈₀ ratio. Finally, DNA was isolated from the organs of control male rats with the newly established DNA isolation protocol for subsequent M₁G analyses. The numbers of M₁G adducts were then compared between the organs and with data from previous reports.

MATERIALS AND METHODS

Materials and instrumentation

Absolute alcohol was purchased from Aaper ethanol (Shelbyville, KY). Other solvents were high-performance liquid chromatography (HPLC) grade and were purchased

from Fisher Scientific (Raleigh, NC). Snap frozen rat tissues were purchased from Taconics (Germantown, NY). Proteinase K, lysis buffer and 70% phenol solutions were purchased from Applied Biosystems (Foster City, CA). Unless stated otherwise, all other chemicals and enzymes were purchased from Sigma-Aldrich Chemical Company (St Louis, MO) and were used without further purification. To prepare homogeneous tissue samples, frozen liver tissues from five control male rats were pooled together and ground into powder using a pre-chilled (−80°C) mortar and pestle. The tissue powder was distributed into small tubes and kept in a −80°C freezer until use.

Quantification of conjugates of M₁G with pentafluorobenzyl hydroxylamine (PFBHA) and its internal standard were performed using a Finnigan Quantum (Thermo, Woburn, MA) triple-quadrupole mass spectrometer connected to the Finnigan Surveyor Micro-LC (Thermo, Woburn, MA).

Effect of antioxidants on M₁G formation during DNA isolation

Method A. DNA was extracted by a procedure described by Gupta (23) with minor modifications. Briefly, 1 g frozen tissue powder was reconstituted in 7 ml homogenization buffer consisting of phosphate-buffered saline (PBS; pH 7.4) with or without an antioxidant. The tissue samples were homogenized with a Tehran homogenizer (Wheaton Instruments, Millville, NJ). After centrifugation at 1000 g for 15 min, the precipitate was washed with 7 ml homogenization buffer. The nuclear fraction was collected by centrifugation and was reconstituted in 6 ml lysis buffer (Applied Biosystems). An RNase mixture (60 µl) consisting of RNase A (80 KeU/ml) and RNase T1 (0.3 U/ml) was added to the tissue lysate, followed by incubation for 1 h at 37°C. Proteinase K (400 U/ml, 60 µl) was added to the samples and they were further incubated for an hour at 50°C. Hydrolyzed protein was then extracted twice with 6 ml of 70% phenol solution (Applied Biosystems) and once with 6 ml chloroform:isoamyl alcohol (49:1, Sevag solution). DNA was precipitated from the aqueous layer by sequential addition of 300 µl 3 M NaCl and 12 ml cold ethanol. After the DNA was collected by centrifugation, the DNA pellet was rinsed with 6 ml of 70% ethanol and air dried on ice. The DNA pellet was resuspended in 500 µl HPLC grade water. DNA samples (25 µl) were mixed with 975 µl of 20 mM Tris-EDTA buffer (pH 8.0) to measure DNA concentration and purity by UV. The DNA solution was stored at −80°C until M₁G analysis. To investigate the artifactual formation of M₁G by oxidation of deoxyribose or lipids during DNA isolation, either butylated hydroxytoluene (BHT), 2,2,6,6-tetramethylpiperidine 1-oxyl

Table 1. Different methods used for DNA isolation from rat liver tissue

Method	Description	Antioxidant	Tissue fraction	Buffering reagent	Protein removal
A	DNA isolation at room temperature	BHT, Tempo, Desferal or Hydroxylamine	Nuclear fraction	Tris	Phenol extraction
B	DNA isolation at low temperature	Tempo, Desferal, Hydroxylamine or PFBHA	Nuclear fraction	Tris	Phenol extraction
C	DNA isolation from tissue homogenate	None	Tissue homogenate	HEPES	Phenol extraction
D	DNA isolation with Tris	Tempo	Nuclear fraction	Tris	Phenol extraction
E	DNA isolation with HEPES	Tempo	Nuclear fraction	HEPES	Phenol extraction
F	DNA isolation with protein precipitation	Tempo	Nuclear fraction	HEPES	Protein precipitation with NaCl
G	DNA isolation with NaI	Tempo	Nuclear fraction	HEPES	Chaotropic reagent (NaI)

(TEMPO), desferal or hydroxylamine was added to the buffer solutions. Homogenization buffer, lysis buffer, 70% phenol and Sevag solutions were supplemented with the additives in the following final concentrations: BHT, 0.01, 0.01, 0.5 and 0.5%; TEMPO, 10, 10, 10 and 10 mM; desferal, 1, 1, 1 and 1 mM; and hydroxylamine, 10, 2, 2 and 2 mM, respectively. To investigate the loss of M₁G during DNA isolation, a positive control sample was prepared by the addition of MDA treated CTD (18) into the nuclear fraction. The concentration of M₁G in the positive control DNA was calculated to be 80 fmol M₁G/100 mg tissue which corresponded to 25 M₁G/10⁸ nt based on a DNA yield of 100 µg/100 mg tissue. Tissue powder (100 mg) was homogenized in 700 µl homogenization buffer and the nuclear fraction was collected and washed as described previously. The nuclear pellet was reconstituted in the lysis buffer followed by the addition of 40 µl MDA-CTD solution (2 fmol M₁G/µl, 0.4 ng DNA/µl). DNA was isolated and stored as described previously. In addition to the antioxidants used for the control tissue, PFBHA was tested and compared for its effect on artifactual formation or loss during DNA isolation. The final concentration for PFBHA in the reagents for DNA isolation was 2 mM.

DNA isolation at low temperature for M₁G adducts measurement

Method B. To investigate the effect of temperature during DNA isolation on the number of M₁G adducts, DNA was extracted from control liver tissue at low temperature (4°C) with a combination of antioxidants, a chelator or alkoxyamines. DNA was extracted by a procedure described by Nakamura and Swenberg (24) with minor modifications. Briefly, the nuclear fraction was prepared from frozen tissue and reconstituted in lysis buffer as described above with pre-chilled solutions and instruments. Proteinase K (400 U/ml, 60 µl) was added to the sample and incubated overnight at 4°C. Hydrolyzed proteins were extracted with phenol extractions and nucleic acids were precipitated by the addition of cold ethanol as detailed previously. The nucleic acid pellet was reconstituted in 2 ml RNA digestion buffer consisting of RNase A (0.8 KeU/ml), RNase T1 (3 mU/ml) and one of the antioxidants in 10 mM HEPES buffer (pH 7.8). The concentration of TEMPO, desferal, hydroxylamine or PFBHA was 1, 0.1, 0.1 or 0.1 mM, respectively. After 1 h incubation at 37°C, DNA was precipitated by the sequential addition of 100 µl of 3 M NaCl and 4 ml cold ethanol. The DNA was collected by centrifugation and rinsed with 70% ethanol. The DNA pellet was reconstituted in 500 µl HPLC grade water.

Comparison of DNA isolation methods for M₁G adducts analysis

To investigate M₁G formation or loss by different types of DNA isolation procedures, DNA was isolated from both control tissue and positive control samples with one of the methods detailed below.

Method C. To investigate the effect of the components within the cell cytosol on M₁G adduct numbers, DNA was isolated from tissue homogenates without nuclear fraction isolation. After the homogenization of tissue in lysis buffer (10 mM HEPES, 1 mM EDTA, 1% SDS and 10 mM TEMPO), RNases and Proteinase K (4 U/ml to final concentration)

were sequentially added to the tissue homogenate. DNA was isolated as described in Method A.

Method D. To investigate the effect of Tris present in DNA isolation reagents on M₁G, DNA was isolated in the presence of TEMPO according to the protocol outlined in Method B and was then analyzed for M₁G adducts.

Frozen tissue powder (3 g) was reconstituted in 21 ml pre-chilled (4°C) homogenization buffer consisting of PBS and 10 mM TEMPO. The nuclear fraction was prepared from tissue homogenization followed by centrifugation. The isolated nuclear fraction was washed with homogenization buffer and reconstituted in 18 ml lysis buffer containing Proteinase K (4 U/ml), 10 mM HEPES, 1 mM EDTA, 1% SDS and 10 mM TEMPO in water. The samples were incubated overnight in a cold room (4°C) with mild shaking. The lysate was distributed to three tubes for DNA isolation via methods E, F and G.

Method E. Hydrolyzed protein was removed by extractions with HEPES-buffered phenol (pH 8.0) and Sevag solution as described in Method B. To prepare the HEPES-buffered phenol, ACS grade phenol was melted at 60°C. An equal volume of 0.1 M HEPES buffer (pH 8.0) was added to the phenol followed by a vigorous mixing for 30 min. The aqueous layer was separated from the phenol mixture after standing for 10 min. After the aqueous layer was replaced with fresh HEPES buffer, the phenol solution was extracted twice with 0.1 M HEPES buffer. The phenol solution was mixed with one-fifth volume of 0.1 M HEPES buffer containing 10 mM TEMPO and was used on the same day as DNA isolation. After the extraction of hydrolyzed proteins with the Sevag solution, nucleic acids were precipitated by sequential additions of NaCl and cold ethanol. The precipitated nucleic acids were collected by centrifugation and washed with 12 ml of 70% ethanol. The remaining ethanol was removed by air on ice for 15 min and the DNA pellet was reconstituted in 2 ml RNase buffer containing RNase A (0.3 KeU/ml), RNase T1 (3 mU/ml) and 10 mM TEMPO in 10 mM HEPES buffer. After an hour of incubation at 37°C, DNA was precipitated by the sequential addition of 100 µl of 3 M NaCl and 4 ml cold ethanol. Afterwards, DNA was collected by centrifugation and rinsed with 70% ethanol. The DNA pellet was resuspended in 500 µl HPLC grade water. DNA concentration was measured and the DNA was stored at -80°C until the M₁G adducts assay.

Method F. In this method, the hydrolyzed proteins were precipitated from the sample by salting out as described previously (25,26) with minor modifications. A 2 ml aliquot of 5 M NaCl was added to the tissue lysate followed by vigorous shaking for 1 min. After incubation on ice for 10 min, the hydrolyzed proteins were removed by centrifugation at 4000 g for 20 min. The supernatant was added to 6 ml isopropanol in a new tube and gently mixed by inversion for 20 min at 4°C. The nucleic acid threads were collected by centrifugation and washed with 12 ml of 70% ethanol. The remaining ethanol was removed by air drying on ice for 15 min and the nucleic acids pellet was reconstituted in 2 ml RNase buffer for subsequent RNA removal followed by DNA precipitation as described in Method E.

Method G. DNA was fractionated with isopropanol in the presence of NaI and SDS as demonstrated in previous studies

(27,28). Tissue lysate (6 ml) was mixed with 12 ml of 6.75 M NaI solution containing 2 mM EDTA, 10 mM TEMPO and 10 mM HEPES (pH 8.0). The sample was mixed by manual inversion followed by the addition of 18 ml isopropanol. The sample was gently mixed in a cold room by an end-over-end mixer for 30 min. The precipitated nucleic acids were collected and washed with 18 ml of 70% ethanol. The following RNA digestion and DNA collection procedures were the same as described previously.

DNA isolation from rat tissues

Liver, kidney, pancreas, lung, heart and brain harvested from five control male rats in the age range of 7–8 months were used to isolate DNA. Nuclear and mitochondrial fractions were separated from liver tissue by using the protocol described by Anson *et al.* (29) with minor modifications. Liver tissues were thawed in seven times volume (v/w) of ice-cold MSHE buffer [0.21 M mannitol, 0.07 M sucrose, 10 mM HEPES (pH 7.4), 1 mM EDTA, 1 mM EGTA and 10 mM TEMPO]. The tissue samples were homogenized with a Tehran homogenizer followed by centrifugation at 50 *g* for 5 min. The supernatant was decanted to the new tube followed by centrifugation at 1000 *g* for 10 min. The precipitated nuclear fraction was washed twice with MSHE buffer and processed for nuclear DNA isolation using Method F. The supernatant was subjected to centrifugation at 9000 *g* for 20 min. The precipitated mitochondrial fraction was washed twice by reconstitution in MSHE buffer followed by centrifugation. The isolated mitochondrial fraction was subjected to DNA isolation using the procedures for DNA isolation from nuclear fraction. The DNA pellet isolated from the mitochondrial fraction was reconstituted in 200 μ l water. Frozen lung or heart tissues were thawed in 10 times volume (v/w) of ice-cold homogenization buffer consisting of 10 mM TEMPO and PBS. The tissue samples were minced with scissors and a tissue tearor (Biospec Products Inc., Bartlesville, OK) followed by homogenization. The procedures for nuclear DNA isolation were the same as those for DNA isolation from liver nuclear DNA. Kidney, pancreas or brain tissue was thawed in seven times volume (v/w) of ice-cold homogenization buffer followed by a homogenization for nuclear fraction isolation. The nuclear fraction was subjected to the protocol used for DNA isolation from liver nuclear fraction.

Analysis of M₁G adducts in DNA

The number of M₁G adducts in sample DNA was determined by the specific derivatization of DNA with PFBHA and LC-MS/MS analysis for the PFBHA-M₁G conjugate similar to the protocol described elsewhere (18). Briefly, 100 μ g of sample DNA was mixed with internal standard DNA (100 fmol ¹⁵N₅-M₁G) in 900 μ l of 2 mM PFBHA solution. After 30 min at 70°C, 100 μ l of 0.1 M HCl was added to the sample mix. After another 30 min at 70°C, the sample was cooled to room temperature. A 10 μ l aliquot was mixed with 90 μ l water and used for purine analysis to measure DNA concentration as described in a previous report (18). The remaining sample was placed on an SPE column (HLB-60, Waters, Milford, MA), that had been preactivated and equilibrated with methanol and water, respectively. The SPE column was washed once with 2 ml water and twice

with 3 ml of 65% methanol. PFBHA-M₁G and the internal standard were eluted with 3 ml of 90% methanol in water. The solvent was removed by vacuum evaporation. The samples were reconstituted in 40 μ l of 10% methanol in water and stored at –80°C until analysis. The samples were separated on an Atlantis d-C18 (3 μ m, 2 mm \times 150 mm, Waters) HPLC column by a gradual increase of acetonitrile. Two specific ion transitions (i.e. *m/z* 401 \rightarrow *m/z* 188 and *m/z* 406 \rightarrow *m/z* 193) were used to detect and quantify PFBHA-M₁G and PFBHA-¹⁵N₅-M₁G, respectively.

Data analysis

The presence of significant differences between mean values was determined by an analysis of variance (ANOVA). The level of statistical significance in all cases was *P* < 0.05.

RESULTS

Effect of antioxidants or work-up temperature on the number of M₁G adducts during DNA isolation

In order to investigate whether there was artifactual formation of M₁G adducts from oxidation of deoxyribose or lipids that could be prevented in part by antioxidants, DNA was prepared from rat liver tissue with or without the addition of antioxidants such as BHT or TEMPO. As shown in Figure 1, supplementing DNA isolation reagents with BHT or TEMPO did not make a statistically significant difference regarding the number of M₁G adducts in DNA compared with the control DNA isolated without an antioxidant. Since desferal, a metal ion chelator, has been shown to significantly reduce the artifactual formation of 8-OH-dG (30), the effects of its presence during DNA isolation on the number of M₁G adducts was tested. In addition, hydroxylamine or PFBHA was tested because they have high reactivity toward MDA and base propenals (i.e. precursors of M₁G). Neither desferal nor alkoxyamines resulted in a statistically significant change in the number of M₁G adducts in the DNA compared with that of control. The effect

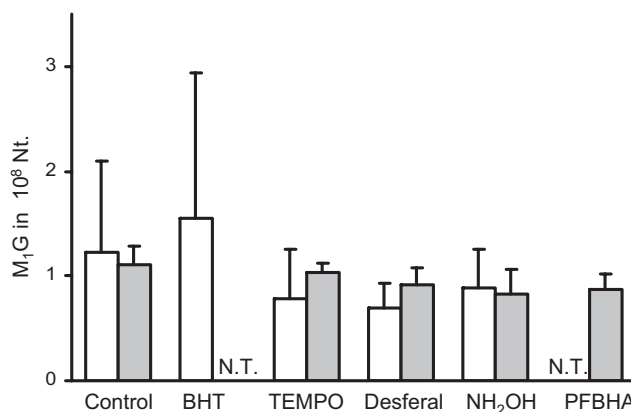


Figure 1. The effect of antioxidants or temperature on the number of M₁G adducts after DNA isolation from control tissue. DNA was isolated from control rat liver tissue with the addition of antioxidant at room temperature (Method A, open rectangles) or at 4°C (Method B, closed rectangles). The number of M₁G adducts in the DNA was quantified with PFBHA labeling for M₁G followed by LC-MS/MS analysis of PFBHA-M₁G conjugates as detailed in the Materials and Methods. Each point represents mean \pm SD from five to six samples for each group. N.T.: not tested.

of a low temperature work-up for DNA isolation has been tested with combinations of different types of antioxidants, a chelator or alkoxyamines. It has been well established that work-up procedures at low temperature significantly reduce the oxidation of unmodified DNA molecules to produce primary oxidative lesions (i.e. 8-OH-dG, single strand breaks and AP sites) during DNA isolation (20,31,32). In contrast to the results for primary oxidative lesions, neither low temperature nor the addition of antioxidant made a significant difference compared with control (Figure 1).

In parallel experiments, the loss of M₁G during DNA isolation was tested using positive control tissue nuclear fractions. Hydroxylamine or PFBHA was reacted with M₁G in DNA to prevent binding with proteins or amines that could result in the reduced recovery of M₁G after DNA isolation. As shown in Figure 2, all additives including hydroxylamine and PFBHA

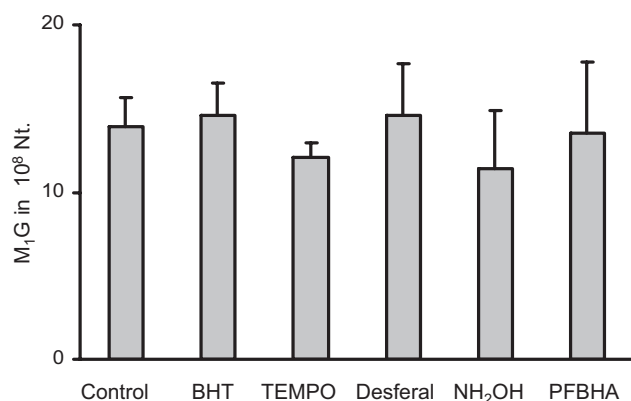


Figure 2. The effect of antioxidants on the number of M₁G adducts after DNA isolation from positive control tissue. DNA was isolated from positive control samples consisting of MDA treated CTD and the nuclear fraction prepared from rat liver tissue. The antioxidants or alkoxyamines were added into the reagents for DNA isolation (Method A). Each point represents mean \pm S.D. from five samples for each group.

had no significant effect on the number of M₁G adducts in the DNA compared with control. Based on the number of M₁G adducts detected in samples, the recovery of positive DNA was $59 \pm 12\%$ from all samples. No statistical significance was observed compared with controls which did not have any additives during DNA isolation.

Comparison of DNA isolation methods for M₁G adducts analysis

Artificial formation or loss of M₁G during DNA isolation was further investigated by a comparison of different DNA isolation protocols. TEMPO was used as an antioxidant because of its solubility in both water and organic solvents. As demonstrated in Figure 3A, DNA isolation from tissue homogenates that did not involve nuclear fraction collection (Method C) resulted in a statistically significant increase in the number of M₁G adducts when compared with DNA isolated from nuclear fraction (Methods D, E, F and G). There was no statistical difference between the other four groups (Methods D, E, F and G) as indicated by the ANOVA. Student *t*-test resulted in a significant difference ($P < 0.05$, two tails) in the number of M₁G between Method C and all other groups. DNA isolation with Tris as a buffering agent did not result in a statistically significant difference in the number of M₁G adducts compared with the result obtained from DNA isolated with HEPES. Two different DNA isolation protocols using NaCl or NaI to remove proteins did not show any statistically significant difference in the number of M₁G adducts when compared with DNA isolation with phenol extraction. In the experiment to isolate DNA from positive control samples, Method C resulted in a significant reduction in the number of M₁G adducts in the DNA compared with Methods E and F. There was no statistically significant difference among the other four groups (Figure 3B).

In addition to M₁G numbers, DNA yields and purities were determined and compared among the different DNA isolation

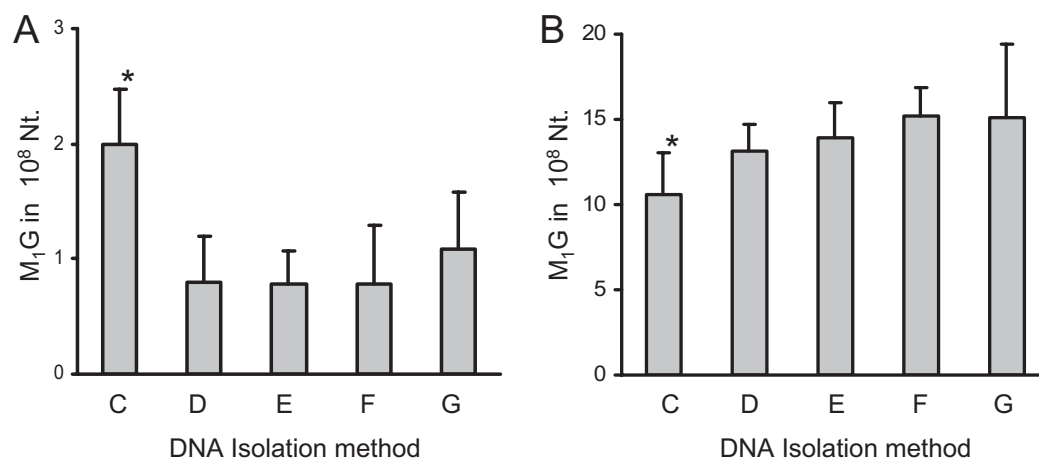


Figure 3. Comparison of DNA isolation methods on the number of M₁G adducts after DNA isolation. DNA was isolated from control (A) or positive control (B) using different types of buffering reagents or methods for the removal of protein. The details regarding DNA isolation are described in the Materials and Methods. Method C: DNA isolation without a preisolation of nuclear fraction, Method D: protein extraction with Tris-buffered phenol, Method E: protein extraction with HEPES-buffered phenol, Method F: protein removal with salting-out, Method G: protein removal with NaI. Each point represents mean \pm SD from five samples for each group. Asterisk, statistically significant difference from other groups ($P < 0.05$).

Table 2. Comparison of DNA yield and purity isolated from control rat liver with different methods

DNA isolation method	A ₂₆₀ /A ₂₈₀	DNA yield based on A ₂₆₀ (mg/g tissue)	Nucleotides (μmol nt/mg DNA)	Calibrated DNA yield (μmol/g tissue)
C	1.79 ± 0.04	0.95 ± 0.04	2.51 ± 0.46	2.40 ± 0.46
D	1.79 ± 0.02	1.00 ± 0.05	2.69 ± 0.10	2.70 ± 0.11
E	1.79 ± 0.03	0.99 ± 0.05	2.45 ± 0.27	2.42 ± 0.29
F	1.80 ± 0.03	0.93 ± 0.01	2.86 ± 0.06 ^a	2.65 ± 0.05
G	1.71 ± 0.02 ^a	0.77 ± 0.09 ^a	2.58 ± 0.40	1.96 ± 0.17 ^a

Each point represents mean ± S.D. from five samples for each group.

^aStatistically significant difference from other groups ($P < 0.05$).

methods. From a visual inspection of DNA pellets and solutions, DNA isolated with Method G was different in color possibly owing to a presence of iodine in the DNA. As detailed in Table 2, Method G resulted in a statistically significant difference in the A₂₆₀/A₂₈₀ ratio compared with that of other DNA isolation methods. The purity tested with UV absorbance (A₂₆₀/A₂₈₀ ratio) for the DNA isolated with Methods C, D, E and F was comparable with 1.8. The phenol extraction methods (Methods C, D and E) produced the best yield. Method F resulted in DNA yields comparable with the phenol extraction methods. However, Method G resulted in significantly decreased yield for DNA recovery compared with other methods. The purity of the DNA was further tested by HPLC analysis for purine bases, as part of the M₁G adducts assay. The number of total bases in each sample was calculated based on A-T and G-C base pairing. The results are described in Table 2. The theoretical value for the number of nucleotides from 100 μg DNA was 302 nmol based on the average molecular weight of dNMP in double-stranded DNA (331: dNMP – H₂O + Na⁺) and assuming a 1:1 ratio of Gua to Ade. The highest yield for purine bases was 2.85 μmol nt/mg DNA, which corresponds to 95% recovery from DNA isolated with Method F. The DNA prepared with Methods C, D, E and G showed significantly lower recovery of purines, which suggests more impurities in those DNA samples. The DNA yield was recalculated from the results of purine analyses. Methods D and F produced the best yield in DNA isolation followed by Methods E and C. The DNA yield from Method G was significantly less than that of the other methods. Based on the result of DNA purity, yield, and the number of M₁G adducts in the DNA, Method F was selected as a standard DNA isolation protocol for the M₁G adducts assay because of consistent results without significant artifact.

DNA isolation from rat tissues

Using Method F, nuclear DNA or mitochondrial DNA was isolated from different tissues of male rats. As shown in Figure 4, mitochondrial DNA from liver tissue showed about a 2-fold greater number of M₁G adducts compared with liver nuclear DNA (1.1 M₁G/10⁸ nt). The nuclear DNA isolated from brain, kidney and pancreas contained a comparable number of M₁G adducts to liver nuclear DNA. However, the nuclear DNA isolated from the lung or heart contained a 1.7- or 3.8-fold greater numbers of M₁G adducts, respectively, compared with liver nuclear DNA.

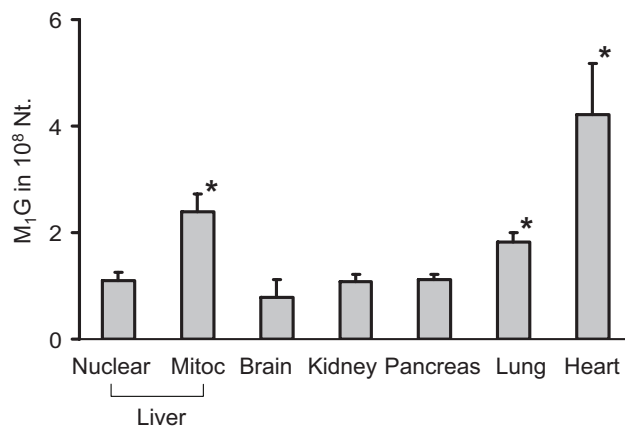


Figure 4. The number of M₁G adducts in liver mitochondrial DNA or nuclear DNA isolated from different rat tissues. Each point represents mean ± SD from four samples for each group. Asterisk, statistically significant difference from liver nuclear DNA ($P < 0.05$).

DISCUSSION

The goal of the present study was to establish a reliable protocol for DNA isolation from animal tissues with the following criteria: (i) to minimize artifactual formation of M₁G from unmodified DNA bases and (ii) to maximize the recovery of M₁G during DNA isolation procedures.

The initial approach to investigating the artifactual formation of M₁G involved determining the effect of antioxidants, a chelating reagent, aldehyde reactive alkoxyamines or different DNA isolation methods on the number of M₁G adducts using rat liver tissue. Transition metals or oxidized phenols have been shown to generate oxygen radicals and probably represent the main mechanism for artifactual increases in oxidative DNA lesions. A number of researchers (20,31,32) examined the protective effects of antioxidants to test the hypothesis that oxidative DNA lesions including 8-OH-dG, aldehydic DNA lesions (ADLs) and strand breaks are artifactually produced during DNA isolation. In addition, low temperature work-up procedures or DNA isolation with non-phenol extraction methods (33) showed significantly lower numbers of 8-OH-dG. However, the results from the present study clearly demonstrate that DNA isolated from the nuclear fraction has consistent numbers of M₁G adducts regardless of which method of isolation is used, and whether or not antioxidants are added. It was hypothesized that the overall process of producing M₁G, compared with primary oxidative DNA lesions, requires more time and ROS in order to produce MDA or precursors to react with Gua. Therefore, the formation of secondary ROS damage is less probable to occur during DNA isolation or sample processing compared to that of primary ROS lesions.

The present study also investigated the loss of M₁G during DNA isolation by introducing protective reagents, such as hydroxylamine and PFBHA, and by comparing with positive control DNA. No statistically significant difference was observed between DNA isolation with or without PFBHA, which suggests that the loss of M₁G during DNA isolation is not a critical issue, at least in the protocols that were used.

To further verify these results, the present study compared M₁G numbers in CTD either purchased from Sigma (St Louis,

MO) or isolated freshly from frozen tissue. The purchased CTD contained orders of magnitude greater numbers of primary oxidative DNA lesions such as 8-OH-dG, AP sites and single strand breaks compared with the carefully isolated CTD (S. Yamaguchi, P. H. Lin, J. Nakamura, S. Liao and J. A. Swenberg, unpublished data). However, the two different CTD had comparable numbers of M₁G adducts.

In an effort to establish the normal range of M₁G adducts *in vivo*, the present study compared different organs regarding the number of M₁G adducts. Surprisingly, the number of M₁G adducts in liver nuclear DNA was 40- to 3000-fold lower than it had been indicated in previous work (12,15–17). The varying numbers of primary oxidative DNA lesions reported by different researchers stem from artifacts during DNA preparation and sample analysis as indicated in the review by Collins *et al.* (34). However, the artifacts during DNA isolation were extensively investigated in this study and turned out to be much less problematic for M₁G adducts analysis. Therefore, the discrepancy between our results and other references with regard to the number of M₁G adducts is most probably owing to different methods of measurement. As detailed previously (18), the novel M₁G adduct assay involving the selective labeling of aldehydic adducts with subsequent LC–MS/MS analysis affords a sensitive and specific means of M₁G adduct measurement. However, some of the values reported in previous references were obtained either from HPLC-fluorescence measurements (15), ³²P-postlabeling (12) or immunoslot assays (17) that may not have been specific enough to measure extremely low amounts of this DNA adduct. Although GC–MS measurement can provide very specific detection of DNA adducts, the artifacts that arise during DNA hydrolysis or derivatization cause a significant increase in the number of oxidative lesions such as 8-OH-dG (31,35). In addition, GC–MS analysis of M₁G adducts (16) after derivatization had interference at low femtomole amounts owing to the noise from the instrument, as mentioned elsewhere (13), which showed an overestimation for the number of M₁G adducts in blank samples as 40 fmol. Therefore, the present study suggests that the numbers of M₁G adducts in genomic DNA have been overestimated owing to the insufficient specificity of previous measurement methods.

Compared with other oxidative DNA lesions such as 8-OH-dG (36), or abasic sites (24), the numbers of M₁G in genomic DNA isolated from rat tissues were one to two orders of magnitude lower in all tissues. These results are consistent with the results from *in vitro* experiments (37) showing that the formation of M₁G was an order of magnitude lower than that for 8-OH-dG or ADLs in ROS reactions with DNA. However, the change in the number of M₁G in the DNA exposed to oxidative conditions was similar to the change in the number of primary ROS lesions (37).

The results regarding the numbers of M₁G adducts in DNA isolated from diverse types of tissues showed a clear difference in the amount of oxidative DNA damage from tissues or cell compartments. The difference in the number of M₁G adducts in the nuclear DNA from six tissues showed that M₁G is related to the amount of ROS production. Rolfe *et al.* (38) reported that the heart uses more oxygen and produces ATP at a faster rate than the liver does. The results from this study were closer to the results regarding ADLs (24) rather than 8-OH-dG reported by other groups (36). This result is in good

agreement with the hypothesis that oxidative DNA sugar damage plays an important role in M₁G formation (37). Consistent with this hypothesis, the number of M₁G adducts was significantly greater in mitochondrial DNA compared with nuclear DNA. It has long been recognized that mitochondrial DNA is more prone to oxidative DNA damage owing to the high amount of ROS (36,39–41). In addition to the high amount of ROS in the mitochondria, the deficiency of nucleotide excision repair in mitochondria could be responsible for the difference in M₁G numbers between mitochondrial DNA and nuclear DNA (42,43) since nucleotide excision repair has been reported to be an important pathway for M₁G repair for nuclear DNA (44).

In conclusion, the results from the present study suggest that M₁G is less prone to oxidation caused by DNA isolation. However, it is still sensitive to ROS damage within living cells. Therefore, M₁G should be a good biomarker for monitoring oxidative DNA damage, which may play a role in numerous genetic diseases including aging and cancer.

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